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SEQUENCE LISTING

<110> Dahlqvist, Andres  
Stahl, Ulf  
Lenman, Marit  
Banas, Antoni  
Ronne, Hans

<120> A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant DNA molecules encoding these enzymes

<130> BASFnae337799RCT1-15

<140> US 09/537,710

<141> 2000-03-30

<150> EP 99106656.4

<151> 1999-04-01

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*B*

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gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp	195	200	205	624
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp	210	215	220	672
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Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
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Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
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Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
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Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
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*WT*

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Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
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Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu  
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Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp  
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Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr  
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Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro  
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Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala  
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Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met  
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Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val

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355 360 365

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*unt*  
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Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly  
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Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr  
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Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn  
595 600 605

His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly  
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Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met  
625 630 635 640

Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val  
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35 40 45

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acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240

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 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly  
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 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile  
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 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly  
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Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile  
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Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala  
 65 70 75 80

Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser  
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Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe  
100 105 110

Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly  
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Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys  
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Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe  
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Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu  
260 265 270

Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val  
275 280 285

Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys  
290 295 300

Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn  
305 310 315 320

Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala  
325 330 335

Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly  
340 345 350

Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu  
355 360 365

Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro

370

375

380

Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser  
385 390 395 400

Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp  
405 410 415

Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp  
420 425 430

Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala  
435 440 445

Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp  
450 455 460

Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile  
465 470 475 480

Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr  
485 490 495

Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp  
500 505 510

Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr  
515 520 525

*b*  
*unit*  
Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr  
530 535 540

Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys  
545 550 555 560

His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu  
565 570 575

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys  
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp  
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn  
610 615 620

<210> 14

<211> 432

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val

1 5 10 15

Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr  
20 25 30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg  
35 40 45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu  
50 55 60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp  
65 70 75 80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met  
85 90 95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly  
100 105 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr  
115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val  
130 135 140

*B*  
*int.*

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu  
145 150 155 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro  
165 170 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu  
180 185 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His  
195 200 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro  
210 215 220

Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro  
225 230 235 240

Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr  
245 250 255

Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg  
260 265 270

Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His  
275 280 285

Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala  
290 295 300

Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val  
305 310 315 320

Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr  
325 330 335

Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro  
340 345 350

Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile  
355 360 365

Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala  
370 375 380

Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His  
385 390 395 400

Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln  
405 410 415

Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu  
420 425 430

*B1*  
<210> 15  
<211> 552  
<212> PRT  
<213> *Arabidopsis thaliana*

<400> 15  
Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala  
1 5 10 15

Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr  
20 25 30

Glu Phe His Gly Asp Tyr Ser Lys Leu Ser Gly Ile Ile Ile Pro Gly  
35 40 45

Phe Ala Ser Thr Gln Leu Arg Ala Trp Ser Ile Leu Asp Cys Pro Tyr  
50 55 60

Thr Pro Leu Asp Phe Asn Pro Leu Asp Leu Val Trp Leu Asp Thr Thr  
65 70 75 80

Lys Leu Leu Ser Ala Val Asn Cys Trp Phe Lys Cys Met Val Leu Asp  
85 90 95

Pro Tyr Asn Gln Thr Asp His Pro Glu Cys Lys Ser Arg Pro Asp Ser  
100 105 110

Gly Leu Ser Ala Ile Thr Glu Leu Asp Pro Gly Tyr Ile Thr Gly Pro  
115 120 125

Leu Ser Thr Val Trp Lys Glu Trp Leu Lys Trp Cys Val Glu Phe Gly  
130 135 140

Ile Glu Ala Asn Ala Ile Val Ala Val Pro Tyr Asp Trp Arg Leu Ser  
145 150 155 160

Pro Thr Lys Leu Glu Glu Arg Asp Leu Tyr Phe His Lys Leu Lys Leu  
165 170 175

Thr Phe Glu Thr Ala Leu Lys Leu Arg Gly Gly Pro Ser Ile Val Phe  
180 185 190

Ala His Ser Met Gly Asn Asn Val Phe Arg Tyr Phe Leu Glu Trp Leu  
195 200 205

Arg Leu Glu Ile Ala Pro Lys His Tyr Leu Lys Trp Leu Asp Gln His  
210 215 220

Ile His Ala Tyr Phe Ala Val Gly Ala Pro Leu Leu Gly Ser Val Glu  
225 230 235 240

*B*  
*unf*

Ala Ile Lys Ser Thr Leu Ser Gly Val Thr Phe Gly Leu Pro Val Ser  
245 250 255

Glu Gly Thr Ala Arg Leu Leu Ser Asn Ser Phe Ala Ser Ser Leu Trp  
260 265 270

Leu Met Pro Phe Ser Lys Asn Cys Lys Gly Asp Asn Thr Phe Trp Thr  
275 280 285

His Phe Ser Gly Gly Ala Ala Lys Lys Asp Lys Arg Val Tyr His Cys  
290 295 300

Asp Glu Glu Glu Tyr Gln Ser Lys Tyr Ser Gly Trp Pro Thr Asn Ile  
305 310 315 320

Ile Asn Ile Glu Ile Pro Ser Thr Ser Ala Arg Glu Leu Ala Asp Gly  
325 330 335

Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met  
340 345 350

Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile  
355 360 365

Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro  
370 375 380

Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val  
385 390 395 400

Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe

405 410 415  
Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile  
420 425 430  
Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val  
435 440 445  
Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His  
450 455 460  
Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr  
465 470 475 480  
Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His  
485 490 495  
Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly  
500 505 510  
Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile  
515 520 525  
Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val  
530 535 540  
Trp Glu Leu Asp Lys Ser Gly Tyr  
545 550

*(b)*  
*cont.*

<210> 1a  
<211> 661  
<212> PRT  
<213> *Saccharomyces cerevisiae*  
  
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1 5 10 15  
  
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
20 25 30  
  
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
35 40 45  
  
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
50 55 60  
  
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
65 70 75 80  
  
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
85 90 95  
  
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe

100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
115 120 125

Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
130 135 140

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
145 150 155 160

Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
180 185 190

Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp  
195 200 205

Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp  
210 215 220

Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn  
225 230 235 240

B  
Unt

Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile  
245 250 255

Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile  
260 265 270

Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys  
290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu  
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp  
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val  
340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly  
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr  
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser  
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser  
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met  
450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu  
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met  
500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr  
515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp  
530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro  
545 550 555 560

Val Phe Leu Thr Glu Asp Gly Thr Val Pro Leu Val Ala His Ser  
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp  
595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser  
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp  
625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln  
645 650 655

Met Pro Phe Pro Met  
660

<210> 2a

<211> 387

<212> PRT

<213> *Arabidopsis thaliana*

<400> 2a

Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro Gly Asn Gly Gly  
1 5 10 15

Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val  
20 25 30

Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp  
35 40 45

Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg  
50 55 60

Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp  
65 70 75 80

Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser  
85 90 95

Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser  
100 105 110

*B*  
*lun4*  
Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val  
115 120 125

Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu  
130 135 140

Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp  
145 150 155 160

Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro  
165 170 175

Val Ile Leu Leu Ser His Ser Leu Gly Leu Phe Val Leu His Phe  
180 185 190

Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe  
195 200 205

Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr  
210 215 220

Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu  
225 230 235 240

Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro  
245 250 255

Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro  
260 265 270

Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile

275

280

285

Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu  
290 295 300

Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly  
305 310 315 320

Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe  
325 330 335

Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn  
340 345 350

Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu  
355 360 365

Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu  
370 375 380

Lys Glu Ile  
385

*B*  
*unx*  
<210> 3a  
<211> 389  
<212> PRT  
<213> Arabidopsis thaliana

<400> 3a  
Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro  
1 5 10 15

Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala  
20 25 30

Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp  
35 40 45

Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly  
50 55 60

Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala  
65 70 75 80

Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile  
85 90 95

Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu  
100 105 110

Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser  
115 120 125

Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile

130

135

140

Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp  
145 150 155 160

Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Pro Asp Trp Cys  
165 170 175

Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly  
180 185 190

Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met  
195 200 205

Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly  
210 215 220

Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn  
225 230 235 240

Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr  
245 250 255

Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile  
260 265 270

*b*  
*WY*  
Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys  
275 280 285

Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val  
290 295 300

Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg  
305 310 315 320

Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser  
325 330 335

Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His  
340 345 350

Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val  
355 360 365

Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser  
370 375 380

Gly Ile Phe Glu Trp  
385

<210> 4a

<211> 1986

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)...(1983)

<400> 4a

atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48  
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser  
1 5 10 15

gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96  
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
20 25 30

aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144  
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
35 40 45

att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192  
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240  
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
65 70 75 80

att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288  
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
85 90 95

ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336  
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
100 105 110

gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384  
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
115 120 125

ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432  
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
130 135 140

tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480  
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
145 150 155 160

aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528  
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
165 170 175

atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576  
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
180 185 190

gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624  
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp

195	200	205			
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp	210	215	220	672	
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn	225	230	235	720	
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile	245	250	255	768	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile	260	265	270	816	
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu	275	280	285	864	
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys	290	295	300	912	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu	305	310	315	320	960
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp	325	330	335		1008
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Arg Gly Trp Val	340	345	350		1056
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly	355	360	365		1104
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr	370	375	380		1152
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser	385	390	395	400	1200
aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser	405	410	415		1248
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct					1296

B  
wt.

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
 420 425 430

tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344  
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
 435 440 445

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392  
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met  
 450 455 460

aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440  
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
 465 470 475 480

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488  
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu  
 485 490 495

gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536  
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met  
 500 505 510

*b*  
*cont*
 gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584  
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr  
 515 520 525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632  
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp  
 530 535 540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680  
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro  
 545 550 555 560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728  
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser  
 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776  
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
 580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824  
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp  
 595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872  
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser  
 610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920  
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp  
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968  
Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln  
645 650 655

atg ccc ttc cca atg taa 1986  
Met Pro Phe Pro Met  
660

<210> 5a  
<211> 661  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 5a  
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser  
1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
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*B*  
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
65 70 75 80

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Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
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Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
115 120 125

Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
130 135 140

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
145 150 155 160

Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
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Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp  
195 200 205

Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp

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215

220

Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn  
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Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile  
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Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile  
260 265 270

Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys  
290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu  
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp  
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Arg Gly Trp Val  
340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly  
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr  
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser  
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser  
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
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Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met  
450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
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Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu  
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met  
500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr  
515 520 525

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Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro  
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Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser  
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
580 585 590

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595 600 605

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gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96  
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
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aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144  
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
35 40 45

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Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
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 65 70 75 80

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 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
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gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384  
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
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ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432  
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gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624  
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp  
 195 200 205

gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg 672  
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp  
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 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile  
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ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt 864  
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
 275 280 285

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 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys  
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gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta 960  
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att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg 1008  
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gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt 1056  
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 340 345 350

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gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc 1152  
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att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca 1200  
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 Met Leu Pro Lys Gly Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
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tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344  
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
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cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392  
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aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440  
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
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gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536  
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 530 535 540

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 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776  
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
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att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824  
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 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968  
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Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
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Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
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Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
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Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
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Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
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Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
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Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
145 150 155 160

Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
180 185 190

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Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp  
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Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn  
225 230 235 240

Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile  
245 250 255

Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile  
260 265 270

Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys  
290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu  
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp  
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val

340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly  
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr  
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser  
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser  
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
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Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
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Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met  
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Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
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Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu  
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met  
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515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp  
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Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser  
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp  
595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser  
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp  
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Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro  
1 5 10 15

ccatct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215  
Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His  
20 25 30

gaa tct tcc aaa tcc cac cat aag naa tcg aac gga gga ggg aag tgg 263  
Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Lys Trp  
35 40 45

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Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr  
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Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro  
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Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly		
20	25	30

tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144  
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130

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 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val  
   35               40                   45  
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly  
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 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile  
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 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly  
   85               90                   95  
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<211> 3896

<212> DNA

<213> *Arabidopsis thaliana*

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aacaagtttgcacaacatt tgaagaagaa agcggaaatga ttcagagag 709

B<sup>1</sup>  
ord.